SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Jaye, Michael C.
Doan, Kim-Anh T.
Krawiec, John A.
Lynch, Kevin J.
Amin, Dilip V.
South, Victoria J.
Marchadier, Dawn
Maugeais, Cyrille
Rader, Daniel J.

(ii) TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR EFFECTING THE LEVELS OF HIGH DENSITY LIPOPROTEIN (HDL) CHOLESTEROL AND APOLIPOPROTEIN AI, VERY LOW DENSITY LIPOPROTEIN (VLDL) CHOLESTEROL AND LOW DENSITY LIPOPROTEIN (LDL) CHOLESTEROL

(iii) NUMBER OF SEQUENCES: 31

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Synnestvedt & Lechner LLP

(B) STREET: Suite 2600 Aramark Tower, 1101 Market Street

(C) CITY: Philadelphia

(D) STATE: PA

(E) COUNTRY: USA

(F) ZIP: 19107

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-Windows 95

(D) SOFTWARE: Corel WordPerfect 8.0 converted to ASCII

(vi) CURRENT APPLICATION DATA:

09/423,860 PCT/US98/09676

(A) APPLICATION NUMBER:

(B) FILING DATE:

(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Kelly, Ph.D., Patrick J.

(B) REGISTRATION NUMBER: 34,638

(C) REFERENCE/DOCKET NUMBER: 22,944 USA

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (215)923-4466

(B) TELEFAX: (215)923-2189

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 367 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 22..180

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
GAATTCGGCT TGATCAATCG C TTC AAA AAG GGG ATC TGT CTG AGC TGC CGC        51
                       Phe Lys Lys Gly Ile Cys Leu Ser Cys Arg
                         1               5                  10

AAG AAC CGT TGT AAT AGC ATT GGC TAC AAT GCC AAG AAA ATG AGG AAC        99
Lys Asn Arg Cys Asn Ser Ile Gly Tyr Asn Ala Lys Lys Met Arg Asn
                 15                  20                  25

AAG AGG AAC AGC AAA ATG TAC CTA AAA ACC CGG GCA GGC ATG CCT TTC       147
Lys Arg Asn Ser Lys Met Tyr Leu Lys Thr Arg Ala Gly Met Pro Phe
             30                  35                  40
```

AGA GGT AAC CTT CAG TCC CTG GAG TGT CCC TGA GGAAGGCCCT TAATACCTCC 200

Arg Gly Asn Leu Gln Ser Leu Glu Cys Pro *

45 50

TTCTTAATAC CATGCTGCAG AGCAGGGCAC ATCCTAGCCC AGGAGAAGTG GCCAGCACAA 260

TCCAATCAAA TCGTTGCAAA TCAGATTACA CTGTGCATGT CCTAGGAAAG GGAATCTTTA 320

CAAAATAAAC AGTGTGGACC CCTCAAAAAA AAAAAAAAGC CGAATTC 367

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Phe Lys Lys Gly Ile Cys Leu Ser Cys Arg Lys Asn Arg Cys Asn Ser

1 5 10 15

Ile Gly Tyr Asn Ala Lys Lys Met Arg Asn Lys Arg Asn Ser Lys Met

20 25 30

Tyr Leu Lys Thr Arg Ala Gly Met Pro Phe Arg Gly Asn Leu Gln Ser

35 40 45

Leu Glu Cys Pro *

50

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1382 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

SUBSTITUTE SHEET (RULE 26)

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 312..1370

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
GAATTCGGCT TCTACTACTA CTAGGCCACG CGTCGCCTAG TACGGGGGGG GGGGGGGGGG      60

TCAGCGAGTC CTTGCCTCCC GGCGGCTCAG GACGAGGGCA GATCTCGTTC TGGGGCAAGC     120

CGTTGACACT CGCTCCCTGC CACCGCCCGG GCTCCGTGCC GCCAAGTTTT CATTTTCCAC     180

CTTCTCTGCC TCCAGTCCCC CAGCCCCTGG CCGAGAGAAG GGTCTTACCG GCCGGGATTG     240

CTGGAAACAC CAAGAGGTGG TTTTTGTTTT TTAAAACTTC TGTTTCTTGG GAGGGGGTGT     300

GGCGGGGCAG G ATG AGC AAC TCC GTT CCT CTG CTC TGT TTC TGG AGC CTC       350
              Met Ser Asn Ser Val Pro Leu Leu Cys Phe Trp Ser Leu
                   55                  60                  65

TGC TAT TGC TTT GCT GCG GGG AGC CCC GTA CCT TTT GGT CCA GAG GGA       398
Cys Tyr Cys Phe Ala Ala Gly Ser Pro Val Pro Phe Gly Pro Glu Gly
              70                  75                  80

CGG CTG GAA GAT AAG CTC CAC AAA CCC AAA GCT ACA CAG ACT GAG GTC       446
Arg Leu Glu Asp Lys Leu His Lys Pro Lys Ala Thr Gln Thr Glu Val
         85                  90                  95

AAA CCA TCT GTG AGG TTT AAC CTC CGC ACC TCC AAG GAC CCA GAG CAT       494
Lys Pro Ser Val Arg Phe Asn Leu Arg Thr Ser Lys Asp Pro Glu His
    100                 105                 110

GAA GGA TGC TAC CTC TCC GTC GGC CAC AGC CAG CCC TTA GAA GAC TGC       542
Glu Gly Cys Tyr Leu Ser Val Gly His Ser Gln Pro Leu Glu Asp Cys
115                 120                 125                 130

AGT TTC AAC ATG ACA GCT AAA ACC TTT TTC ATC ATT CAC GGA TGG ACG       590
Ser Phe Asn Met Thr Ala Lys Thr Phe Phe Ile Ile His Gly Trp Thr
                135                 140                 145
```

```
ATG AGC GGT ATC TTT GAA AAC TGG CTG CAC AAA CTC GTG TCA GCC CTG        638
Met Ser Gly Ile Phe Glu Asn Trp Leu His Lys Leu Val Ser Ala Leu
            150                 155                 160
CAC ACA AGA GAG AAA GAC GCC AAT GTA GTT GTG GTT GAC TGG CTC CCC        686
His Thr Arg Glu Lys Asp Ala Asn Val Val Val Val Asp Trp Leu Pro
        165                 170                 175
CTG GCC CAC CAG CTT TAC ACG GAT GCG GTC AAT AAT ACC AGG GTG GTG        734
Leu Ala His Gln Leu Tyr Thr Asp Ala Val Asn Asn Thr Arg Val Val
    180                 185                 190
GGA CAC AGC ATT GCC AGG ATG CTC GAC TGG CTG CAG GAG AAG GAC GAT        782
Gly His Ser Ile Ala Arg Met Leu Asp Trp Leu Gln Glu Lys Asp Asp
195                 200                 205                 210
TTT TCT CTC GGG AAT GTC CAC TTG ATC GGC TAC AGC CTC GGA GCG CAC        830
Phe Ser Leu Gly Asn Val His Leu Ile Gly Tyr Ser Leu Gly Ala His
                215                 220                 225
GTG GCC GGG TAT GCA GGC AAC TTC GTG AAA GGA ACG GTG GGC CGA ATC        878
Val Ala Gly Tyr Ala Gly Asn Phe Val Lys Gly Thr Val Gly Arg Ile
            230                 235                 240
ACA GGT TTG GAT CCT GCC GGG CCC ATG TTT GAA GGG GCC GAC ATC CAC        926
Thr Gly Leu Asp Pro Ala Gly Pro Met Phe Glu Gly Ala Asp Ile His
        245                 250                 255
AAG AGG CTC TCT CCG GAC GAT GCA GAT TTT GTG GAT GTC CTC CAC ACC        974
Lys Arg Leu Ser Pro Asp Asp Ala Asp Phe Val Asp Val Leu His Thr
    260                 265                 270
TAC ACG CGT TCC TTC GGC TTG AGC ATT GGT ATT CAG ATG CCT GTG GGC       1022
Tyr Thr Arg Ser Phe Gly Leu Ser Ile Gly Ile Gln Met Pro Val Gly
275                 280                 285                 290
CAC ATT GAC ATC TAC CCC AAT GGG GGT GAC TTC CAG CCA GGC TGT GGA       1070
His Ile Asp Ile Tyr Pro Asn Gly Gly Asp Phe Gln Pro Gly Cys Gly
                295                 300                 305
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CTC AAC GAT GTC TTG GGA TCA ATT GCA TAT GGA ACA ATC ACA GAG GTG      1118
Leu Asn Asp Val Leu Gly Ser Ile Ala Tyr Gly Thr Ile Thr Glu Val
            310                 315                 320

GTA AAA TGT GAG CAT GAG CGA GCC GTC CAC CTC TTT GTT GAC TCT CTG      1166
Val Lys Cys Glu His Glu Arg Ala Val His Leu Phe Val Asp Ser Leu
        325                 330                 335

GTG AAT CAG GAC AAG CCG AGT TTT GCC TTC CAG TGC ACT GAC TCC AAT      1214
Val Asn Gln Asp Lys Pro Ser Phe Ala Phe Gln Cys Thr Asp Ser Asn
    340                 345                 350

CGC TTC AAA AAG GGG ATC TGT CTG AGC TGC CGC AAG AAC CGT TGT AAT      1262
Arg Phe Lys Lys Gly Ile Cys Leu Ser Cys Arg Lys Asn Arg Cys Asn
355                 360                 365                 370

AGC ATT GGC TAC AAT GCC AAG AAA ATG AGG AAC AAG AGG AAC AGC AAA      1310
Ser Ile Gly Tyr Asn Ala Lys Lys Met Arg Asn Lys Arg Asn Ser Lys
                375                 380                 385

ATG TAC CTA AAA ACC CGG GCA GGC ATG CCT TTC AGA GGT AAC CTT CAG      1358
Met Tyr Leu Lys Thr Arg Ala Gly Met Pro Phe Arg Gly Asn Leu Gln
            390                 395                 400

TCC CTG GAG TGT CAAGCCGAAT TC                                       1382
Ser Leu Glu Cys
        405
```

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 353 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
Met Ser Asn Ser Val Pro Leu Leu Cys Phe Trp Ser Leu Cys Tyr Cys
 1               5                  10                  15
Phe Ala Ala Gly Ser Pro Val Pro Phe Gly Pro Glu Gly Arg Leu Glu
            20                  25                  30
Asp Lys Leu His Lys Pro Lys Ala Thr Gln Thr Glu Val Lys Pro Ser
        35                  40                  45
Val Arg Phe Asn Leu Arg Thr Ser Lys Asp Pro Glu His Glu Gly Cys
    50                  55                  60
Tyr Leu Ser Val Gly His Ser Gln Pro Leu Glu Asp Cys Ser Phe Asn
65                  70                  75                  80
Met Thr Ala Lys Thr Phe Phe Ile Ile His Gly Trp Thr Met Ser Gly
                85                  90                  95
Ile Phe Glu Asn Trp Leu His Lys Leu Val Ser Ala Leu His Thr Arg
            100                 105                 110
Glu Lys Asp Ala Asn Val Val Val Val Asp Trp Leu Pro Leu Ala His
        115                 120                 125
Gln Leu Tyr Thr Asp Ala Val Asn Asn Thr Arg Val Val Gly His Ser
    130                 135                 140
Ile Ala Arg Met Leu Asp Trp Leu Gln Glu Lys Asp Asp Phe Ser Leu
145                 150                 155                 160
Gly Asn Val His Leu Ile Gly Tyr Ser Leu Gly Ala His Val Ala Gly
                165                 170                 175
Tyr Ala Gly Asn Phe Val Lys Gly Thr Val Gly Arg Ile Thr Gly Leu
            180                 185                 190
Asp Pro Ala Gly Pro Met Phe Glu Gly Ala Asp Ile His Lys Arg Leu
        195                 200                 205
Ser Pro Asp Asp Ala Asp Phe Val Asp Val Leu His Thr Tyr Thr Arg
    210                 215                 220
```

SUBSTITUTE SHEET (RULE 26)

```
Ser Phe Gly Leu Ser Ile Gly Ile Gln Met Pro Val Gly His Ile Asp
225                 230                 235                 240
Ile Tyr Pro Asn Gly Gly Asp Phe Gln Pro Gly Cys Gly Leu Asn Asp
                245                 250                 255
Val Leu Gly Ser Ile Ala Tyr Gly Thr Ile Thr Glu Val Val Lys Cys
            260                 265                 270
Glu His Glu Arg Ala Val His Leu Phe Val Asp Ser Leu Val Asn Gln
        275                 280                 285
Asp Lys Pro Ser Phe Ala Phe Gln Cys Thr Asp Ser Asn Arg Phe Lys
    290                 295                 300
Lys Gly Ile Cys Leu Ser Cys Arg Lys Asn Arg Cys Asn Ser Ile Gly
305                 310                 315                 320
Tyr Asn Ala Lys Lys Met Arg Asn Lys Arg Asn Ser Lys Met Tyr Leu
                325                 330                 335
Lys Thr Arg Ala Gly Met Pro Phe Arg Gly Asn Leu Gln Ser Leu Glu
            340                 345                 350
Cys
```

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1065 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..1065

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```
ATG AGC AAC TCC GTT CCT CTG CTC TGT TTC TGG AGC CTC TGC TAT TGC        48
Met Ser Asn Ser Val Pro Leu Leu Cys Phe Trp Ser Leu Cys Tyr Cys
    355                 360                 365

TTT GCT GCG GGG AGC CCC GTA CCT TTT GGT CCA GAG GGA CGG CTG GAA        96
Phe Ala Ala Gly Ser Pro Val Pro Phe Gly Pro Glu Gly Arg Leu Glu
370                 375                 380                 385

GAT AAG CTC CAC AAA CCC AAA GCT ACA CAG ACT GAG GTC AAA CCA TCT       144
Asp Lys Leu His Lys Pro Lys Ala Thr Gln Thr Glu Val Lys Pro Ser
                390                 395                 400

GTG AGG TTT AAC CTC CGC ACC TCC AAG GAC CCA GAG CAT GAA GGA TGC       192
Val Arg Phe Asn Leu Arg Thr Ser Lys Asp Pro Glu His Glu Gly Cys
            405                 410                 415

TAC CTC TCC GTC GGC CAC AGC CAG CCC TTA GAA GAC TGC AGT TTC AAC       240
Tyr Leu Ser Val Gly His Ser Gln Pro Leu Glu Asp Cys Ser Phe Asn
        420                 425                 430

ATG ACA GCT AAA ACC TTT TTC ATC ATT CAC GGA TGG ACG ATG AGC GGT       288
Met Thr Ala Lys Thr Phe Phe Ile Ile His Gly Trp Thr Met Ser Gly
    435                 440                 445

ATC TTT GAA AAC TGG CTG CAC AAA CTC GTG TCA GCC CTG CAC ACA AGA       336
Ile Phe Glu Asn Trp Leu His Lys Leu Val Ser Ala Leu His Thr Arg
450                 455                 460                 465

GAG AAA GAC GCC AAT GTA GTT GTG GTT GAC TGG CTC CCC CTG GCC CAC       384
Glu Lys Asp Ala Asn Val Val Val Val Asp Trp Leu Pro Leu Ala His
                470                 475                 480

CAG CTT TAC ACG GAT GCG GTC AAT AAT ACC AGG GTG GTG GGA CAC AGC       432
Gln Leu Tyr Thr Asp Ala Val Asn Asn Thr Arg Val Val Gly His Ser
            485                 490                 495
```

```
ATT GCC AGG ATG CTC GAC TGG CTG CAG GAG AAG GAC GAT TTT TCT CTC        480
Ile Ala Arg Met Leu Asp Trp Leu Gln Glu Lys Asp Asp Phe Ser Leu
        500                 505                 510
GGG AAT GTC CAC TTG ATC GGC TAC AGC CTC GGA GCG CAC GTG GCC GGG        528
Gly Asn Val His Leu Ile Gly Tyr Ser Leu Gly Ala His Val Ala Gly
    515                 520                 525
TAT GCA GGC AAC TTC GTG AAA GGA ACG GTG GGC CGA ATC ACA GGT TTG        576
Tyr Ala Gly Asn Phe Val Lys Gly Thr Val Gly Arg Ile Thr Gly Leu
530                 535                 540                 545
GAT CCT GCC GGG CCC ATG TTT GAA GGG GCC GAC ATC CAC AAG AGG CTC        624
Asp Pro Ala Gly Pro Met Phe Glu Gly Ala Asp Ile His Lys Arg Leu
                550                 555                 560
TCT CCG GAC GAT GCA GAT TTT GTG GAT GTC CTC CAC ACC TAC ACG CGT        672
Ser Pro Asp Asp Ala Asp Phe Val Asp Val Leu His Thr Tyr Thr Arg
            565                 570                 575
TCC TTC GGC TTG AGC ATT GGT ATT CAG ATG CCT GTG GGC CAC ATT GAC        720
Ser Phe Gly Leu Ser Ile Gly Ile Gln Met Pro Val Gly His Ile Asp
        580                 585                 590
ATC TAC CCC AAT GGG GGT GAC TTC CAG CCA GGC TGT GGA CTC AAC GAT        768
Ile Tyr Pro Asn Gly Gly Asp Phe Gln Pro Gly Cys Gly Leu Asn Asp
    595                 600                 605
GTC TTG GGA TCA ATT GCA TAT GGA ACA ATC ACA GAG GTG GTA AAA TGT        816
Val Leu Gly Ser Ile Ala Tyr Gly Thr Ile Thr Glu Val Val Lys Cys
610                 615                 620                 625
GAG CAT GAG CGA GCC GTC CAC CTC TTT GTT GAC TCT CTG GTG AAT CAG        864
Glu His Glu Arg Ala Val His Leu Phe Val Asp Ser Leu Val Asn Gln
                630                 635                 640
GAC AAG CCG AGT TTT GCC TTC CAG TGC ACT GAC TCC AAT CGC TTC AAA        912
Asp Lys Pro Ser Phe Ala Phe Gln Cys Thr Asp Ser Asn Arg Phe Lys
            645                 650                 655
```

```
AAG GGG ATC TGT CTG AGC TGC CGC AAG AAC CGT TGT AAT AGC ATT GGC      960
Lys Gly Ile Cys Leu Ser Cys Arg Lys Asn Arg Cys Asn Ser Ile Gly
        660                 665                 670
TAC AAT GCC AAG AAA ATG AGG AAC AAG AGG AAC AGC AAA ATG TAC CTA     1008
Tyr Asn Ala Lys Lys Met Arg Asn Lys Arg Asn Ser Lys Met Tyr Leu
    675                 680                 685
AAA ACC CGG GCA GGC ATG CCT TTC AGA GGT AAC CTT CAG TCC CTG GAG     1056
Lys Thr Arg Ala Gly Met Pro Phe Arg Gly Asn Leu Gln Ser Leu Glu
690                 695                 700                 705
TGT CCC TGA                                                        1065
Cys Pro  *
```

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 355 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```
Met Ser Asn Ser Val Pro Leu Leu Cys Phe Trp Ser Leu Cys Tyr Cys
  1               5                  10                  15
Phe Ala Ala Gly Ser Pro Val Pro Phe Gly Pro Glu Gly Arg Leu Glu
            20                  25                  30
Asp Lys Leu His Lys Pro Lys Ala Thr Gln Thr Glu Val Lys Pro Ser
        35                  40                  45
Val Arg Phe Asn Leu Arg Thr Ser Lys Asp Pro Glu His Glu Gly Cys
    50                  55                  60
Tyr Leu Ser Val Gly His Ser Gln Pro Leu Glu Asp Cys Ser Phe Asn
65                  70                  75                  80
```

Met Thr Ala Lys Thr Phe Phe Ile Ile His Gly Trp Thr Met Ser Gly
85 90 95
Ile Phe Glu Asn Trp Leu His Lys Leu Val Ser Ala Leu His Thr Arg
100 105 110
Glu Lys Asp Ala Asn Val Val Val Val Asp Trp Leu Pro Leu Ala His
115 120 125
Gln Leu Tyr Thr Asp Ala Val Asn Asn Thr Arg Val Val Gly His Ser
130 135 140
Ile Ala Arg Met Leu Asp Trp Leu Gln Glu Lys Asp Asp Phe Ser Leu
145 150 155 160
Gly Asn Val His Leu Ile Gly Tyr Ser Leu Gly Ala His Val Ala Gly
165 170 175
Tyr Ala Gly Asn Phe Val Lys Gly Thr Val Gly Arg Ile Thr Gly Leu
180 185 190
Asp Pro Ala Gly Pro Met Phe Glu Gly Ala Asp Ile His Lys Arg Leu
195 200 205
Ser Pro Asp Asp Ala Asp Phe Val Asp Val Leu His Thr Tyr Thr Arg
210 215 220
Ser Phe Gly Leu Ser Ile Gly Ile Gln Met Pro Val Gly His Ile Asp
225 230 235 240
Ile Tyr Pro Asn Gly Gly Asp Phe Gln Pro Gly Cys Gly Leu Asn Asp
245 250 255
Val Leu Gly Ser Ile Ala Tyr Gly Thr Ile Thr Glu Val Val Lys Cys
260 265 270
Glu His Glu Arg Ala Val His Leu Phe Val Asp Ser Leu Val Asn Gln
275 280 285
Asp Lys Pro Ser Phe Ala Phe Gln Cys Thr Asp Ser Asn Arg Phe Lys
290 295 300
Lys Gly Ile Cys Leu Ser Cys Arg Lys Asn Arg Cys Asn Ser Ile Gly
305 310 315 320

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Tyr Asn Ala Lys Lys Met Arg Asn Lys Arg Asn Ser Lys Met Tyr Leu
325 330 335

Lys Thr Arg Ala Gly Met Pro Phe Arg Gly Asn Leu Gln Ser Leu Glu
340 345 350

Cys Pro *
355

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2565 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 252..1754

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAATTCGCGG CCGCGTCGAC GGCGGCTCAG GACGAGGGCA GATCTCGTTC TGGGGCAAGC 60

CGTTGACACT CGCTCCCTGC CACCGCCCGG GCTCCGTGCC GCCAAGTTTT CATTTTCCAC 120

CTTCTCTGCC TCCAGTCCCC CAGCCCCTGG CCGAGAGAAG GGTCTTACCG GCCGGGATTG 180

CTGGAAACAC CAAGAGGTGG TTTTTGTTTT TTAAAACTTC TGTTTCTTGG GAGGGGGTGT 240

GGCGGGGCAG G ATG AGC AAC TCC GTT CCT CTG CTC TGT TTC TGG AGC CTC 290
Met Ser Asn Ser Val Pro Leu Leu Cys Phe Trp Ser Leu
360 365

TGC TAT TGC TTT GCT GCG GGG AGC CCC GTA CCT TTT GGT CCA GAG GGA 338
Cys Tyr Cys Phe Ala Ala Gly Ser Pro Val Pro Phe Gly Pro Glu Gly
370 375 380

```
CGG CTG GAA GAT AAG CTC CAC AAA CCC AAA GCT ACA CAG ACT GAG GTC      386
Arg Leu Glu Asp Lys Leu His Lys Pro Lys Ala Thr Gln Thr Glu Val
385                 390                 395                 400
AAA CCA TCT GTG AGG TTT AAC CTC CGC ACC TCC AAG GAC CCA GAG CAT      434
Lys Pro Ser Val Arg Phe Asn Leu Arg Thr Ser Lys Asp Pro Glu His
                405                 410                 415
GAA GGA TGC TAC CTC TCC GTC GGC CAC AGC CAG CCC TTA GAA GAC TGC      482
Glu Gly Cys Tyr Leu Ser Val Gly His Ser Gln Pro Leu Glu Asp Cys
            420                 425                 430
AGT TTC AAC ATG ACA GCT AAA ACC TTT TTC ATC ATT CAC GGA TGG ACG      530
Ser Phe Asn Met Thr Ala Lys Thr Phe Phe Ile Ile His Gly Trp Thr
        435                 440                 445
ATG AGC GGT ATC TTT GAA AAC TGG CTG CAC AAA CTC GTG TCA GCC CTG      578
Met Ser Gly Ile Phe Glu Asn Trp Leu His Lys Leu Val Ser Ala Leu
    450                 455                 460
CAC ACA AGA GAG AAA GAC GCC AAT GTA GTT GTG GTT GAC TGG CTC CCC      626
His Thr Arg Glu Lys Asp Ala Asn Val Val Val Val Asp Trp Leu Pro
465                 470                 475                 480
CTG GCC CAC CAG CTT TAC ACG GAT GCG GTC AAT AAT ACC AGG GTG GTG      674
Leu Ala His Gln Leu Tyr Thr Asp Ala Val Asn Asn Thr Arg Val Val
                485                 490                 495
GGA CAC AGC ATT GCC AGG ATG CTC GAC TGG CTG CAG GAG AAG GAC GAT      722
Gly His Ser Ile Ala Arg Met Leu Asp Trp Leu Gln Glu Lys Asp Asp
            500                 505                 510
TTT TCT CTC GGG AAT GTC CAC TTG ATC GGC TAC AGC CTC GGA GCG CAC      770
Phe Ser Leu Gly Asn Val His Leu Ile Gly Tyr Ser Leu Gly Ala His
        515                 520                 525
GTG GCC GGG TAT GCA GGC AAC TTC GTG AAA GGA ACG GTG GGC CGA ATC      818
Val Ala Gly Tyr Ala Gly Asn Phe Val Lys Gly Thr Val Gly Arg Ile
    530                 535                 540
```

0294E0E0.0295.0

```
ACA GGT TTG GAT CCT GCC GGG CCC ATG TTT GAA GGG GCC GAC ATC CAC       866
Thr Gly Leu Asp Pro Ala Gly Pro Met Phe Glu Gly Ala Asp Ile His
545                 550                 555                 560
AAG AGG CTC TCT CCG GAC GAT GCA GAT TTT GTG GAT GTC CTC CAC ACC      914
Lys Arg Leu Ser Pro Asp Asp Ala Asp Phe Val Asp Val Leu His Thr
                565                 570                 575
TAC ACG CGT TCC TTC GGC TTG AGC ATT GGT ATT CAG ATG CCT GTG GGC       962
Tyr Thr Arg Ser Phe Gly Leu Ser Ile Gly Ile Gln Met Pro Val Gly
            580                 585                 590
CAC ATT GAC ATC TAC CCC AAT GGG GGT GAC TTC CAG CCA GGC TGT GGA      1010
His Ile Asp Ile Tyr Pro Asn Gly Gly Asp Phe Gln Pro Gly Cys Gly
        595                 600                 605
CTC AAC GAT GTC TTG GGA TCA ATT GCA TAT GGA ACA ATC ACA GAG GTG      1058
Leu Asn Asp Val Leu Gly Ser Ile Ala Tyr Gly Thr Ile Thr Glu Val
    610                 615                 620
GTA AAA TGT GAG CAT GAG CGA GCC GTC CAC CTC TTT GTT GAC TCT CTG      1106
Val Lys Cys Glu His Glu Arg Ala Val His Leu Phe Val Asp Ser Leu
625                 630                 635                 640
GTG AAT CAG GAC AAG CCG AGT TTT GCC TTC CAG TGC ACT GAC TCC AAT      1154
Val Asn Gln Asp Lys Pro Ser Phe Ala Phe Gln Cys Thr Asp Ser Asn
                645                 650                 655
CGC TTC AAA AAG GGG ATC TGT CTG AGC TGC CGC AAG AAC CGT TGT AAT      1202
Arg Phe Lys Lys Gly Ile Cys Leu Ser Cys Arg Lys Asn Arg Cys Asn
            660                 665                 670
AGC ATT GGC TAC AAT GCC AAG AAA ATG AGG AAC AAG AGG AAC AGC AAA      1250
Ser Ile Gly Tyr Asn Ala Lys Lys Met Arg Asn Lys Arg Asn Ser Lys
        675                 680                 685
ATG TAC CTA AAA ACC CGG GCA GGC ATG CCT TTC AGA GTT TAC CAT TAT      1298
Met Tyr Leu Lys Thr Arg Ala Gly Met Pro Phe Arg Val Tyr His Tyr
    690                 695                 700
```

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```
CAG ATG AAA ATC CAT GTC TTC AGT TAC AAG AAC ATG GGA GAA ATT GAG      1346
Gln Met Lys Ile His Val Phe Ser Tyr Lys Asn Met Gly Glu Ile Glu
705                 710                 715                 720
CCC ACC TTT TAC GTC ACC CTT TAT GGC ACT AAT GCA GAT TCC CAG ACT      1394
Pro Thr Phe Tyr Val Thr Leu Tyr Gly Thr Asn Ala Asp Ser Gln Thr
                725                 730                 735
CTG CCA CTG GAA ATA GTG GAG CGG ATC GAG CAG AAT GCC ACC AAC ACC      1442
Leu Pro Leu Glu Ile Val Glu Arg Ile Glu Gln Asn Ala Thr Asn Thr
            740                 745                 750
TTC CTG GTC TAC ACC GAG GAG GAC TTG GGA GAC CTC TTG AAG ATC CAG      1490
Phe Leu Val Tyr Thr Glu Glu Asp Leu Gly Asp Leu Leu Lys Ile Gln
        755                 760                 765
CTC ACC TGG GAG GGG GCC TCT CAG TCT TGG TAC AAC CTG TGG AAG GAG      1538
Leu Thr Trp Glu Gly Ala Ser Gln Ser Trp Tyr Asn Leu Trp Lys Glu
    770                 775                 780
TTT CGC AGC TAC CTG TCT CAA CCC CGC AAC CCC GGA CGG GAG CTG AAT      1586
Phe Arg Ser Tyr Leu Ser Gln Pro Arg Asn Pro Gly Arg Glu Leu Asn
785                 790                 795                 800
ATC AGG CGC ATC CGG GTG AAG TCT GGG GAA ACC CAG CGG AAA CTG ACA      1634
Ile Arg Arg Ile Arg Val Lys Ser Gly Glu Thr Gln Arg Lys Leu Thr
                805                 810                 815
TTT TGT ACA GAA GAC CCT GAG AAC ACC AGC ATA TCC CCA GGC CGG GAG      1682
Phe Cys Thr Glu Asp Pro Glu Asn Thr Ser Ile Ser Pro Gly Arg Glu
            820                 825                 830
CTC TGG TTT CGC AAG TGT CGG GAT GGC TGG AGG ATG AAA AAC GAA ACC      1730
Leu Trp Phe Arg Lys Cys Arg Asp Gly Trp Arg Met Lys Asn Glu Thr
        835                 840                 845
AGT CCC ACT GTG GAG CTT CCC TGA GGGTGCCCGG GCAAGTCTTG CCAGCAAGGC      1784
Ser Pro Thr Val Glu Leu Pro  *
    850                 855
```

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AGCAAGACTT CCTGCTATCC AAGCCCATGG AGGAAAGTTA CTGCTGAGGA CCCACCCAAT 1844

GGAAGGATTC TTCTCAGCCT TGACCCTGGA GCACTGGGAA CAACTGGTCT CCTGTGATGG 1904

CTGGGACTCC TCGCGGGAGG GGACTGCGCT GCTATAGCTC TTGCTGCCTC TCTTGAATAG 1964

CTCTAACTCC AAACCTCTGT CCACACCTCC AGAGCACCAA GTCCAGATTT GTGTGTAAGC 2024

AGCTGGGTGC CTGGGGCCTC TCGTGCACAC TGGATTGGTT TCTCAGTTGC TGGGCGAGCC 2084

TGTACTCTGC CTGACGAGGA ACGCTGGCTC CGAAGAGGCC CTGTGTAGAA GGCTGTCAGC 2144

TGCTCAGCCT GCTTTGAGCC TCAGTGAGAA GTCCTTCCGA CAGGAGCTGA CTCATGTCAG 2204

GATGGCAGGC CTGGTATCTT GCTCGGGCCC TGGCTGTTGG GGTTCTCATG GGTTGCACTG 2264

ACCATACTGC TTACGTCTTA GCCATTCCGT CCTGCTCCCC AGCTCACTCT CTGAAGCACA 2324

CATCATTGGC TTTCCTATTT TTCTGTTCAT TTTTTAATTG AGCAAATGTC TATTGAACAC 2384

TTAAAATTAA TTAGAATGTG GTAATGGACA TATTACTGAG CCTCTCCATT TGGAACCCAG 2444

TGGAGTTGGG ATTTCTAGAC CCTCTTTCTG TTTGGATGGT GTATGTGTAT ATGCATGGGG 2504

AAAGGCACCT GGGGCCTGGG GGAGGCTATA GGATATAAGC AGTCGACGCG GCCGCGAATT 2564

C 2565

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 501 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Ser Asn Ser Val Pro Leu Leu Cys Phe Trp Ser Leu Cys Tyr Cys

1 5 10 15

Phe Ala Ala Gly Ser Pro Val Pro Phe Gly Pro Glu Gly Arg Leu Glu

20 25 30

Asp Lys Leu His Lys Pro Lys Ala Thr Gln Thr Glu Val Lys Pro Ser

35 40 45

Val Arg Phe Asn Leu Arg Thr Ser Lys Asp Pro Glu His Glu Gly Cys

50 55 60

Tyr Leu Ser Val Gly His Ser Gln Pro Leu Glu Asp Cys Ser Phe Asn
65 70 75 80
Met Thr Ala Lys Thr Phe Phe Ile Ile His Gly Trp Thr Met Ser Gly
85 90 95
Ile Phe Glu Asn Trp Leu His Lys Leu Val Ser Ala Leu His Thr Arg
100 105 110
Glu Lys Asp Ala Asn Val Val Val Val Asp Trp Leu Pro Leu Ala His
115 120 125
Gln Leu Tyr Thr Asp Ala Val Asn Asn Thr Arg Val Val Gly His Ser
130 135 140
Ile Ala Arg Met Leu Asp Trp Leu Gln Glu Lys Asp Asp Phe Ser Leu
145 150 155 160
Gly Asn Val His Leu Ile Gly Tyr Ser Leu Gly Ala His Val Ala Gly
165 170 175
Tyr Ala Gly Asn Phe Val Lys Gly Thr Val Gly Arg Ile Thr Gly Leu
180 185 190
Asp Pro Ala Gly Pro Met Phe Glu Gly Ala Asp Ile His Lys Arg Leu
195 200 205
Ser Pro Asp Asp Ala Asp Phe Val Asp Val Leu His Thr Tyr Thr Arg
210 215 220
Ser Phe Gly Leu Ser Ile Gly Ile Gln Met Pro Val Gly His Ile Asp
225 230 235 240
Ile Tyr Pro Asn Gly Gly Asp Phe Gln Pro Gly Cys Gly Leu Asn Asp
245 250 255
Val Leu Gly Ser Ile Ala Tyr Gly Thr Ile Thr Glu Val Val Lys Cys
260 265 270
Glu His Glu Arg Ala Val His Leu Phe Val Asp Ser Leu Val Asn Gln
275 280 285
Asp Lys Pro Ser Phe Ala Phe Gln Cys Thr Asp Ser Asn Arg Phe Lys
290 295 300

```
Lys Gly Ile Cys Leu Ser Cys Arg Lys Asn Arg Cys Asn Ser Ile Gly
305                 310                 315                 320
Tyr Asn Ala Lys Lys Met Arg Asn Lys Arg Asn Ser Lys Met Tyr Leu
                    325                 330                 335
Lys Thr Arg Ala Gly Met Pro Phe Arg Val Tyr His Tyr Gln Met Lys
            340                 345                 350
Ile His Val Phe Ser Tyr Lys Asn Met Gly Glu Ile Glu Pro Thr Phe
        355                 360                 365
Tyr Val Thr Leu Tyr Gly Thr Asn Ala Asp Ser Gln Thr Leu Pro Leu
    370                 375                 380
Glu Ile Val Glu Arg Ile Glu Gln Asn Ala Thr Asn Thr Phe Leu Val
385                 390                 395                 400
Tyr Thr Glu Glu Asp Leu Gly Asp Leu Leu Lys Ile Gln Leu Thr Trp
                405                 410                 415
Glu Gly Ala Ser Gln Ser Trp Tyr Asn Leu Trp Lys Glu Phe Arg Ser
            420                 425                 430
Tyr Leu Ser Gln Pro Arg Asn Pro Gly Arg Glu Leu Asn Ile Arg Arg
        435                 440                 445
Ile Arg Val Lys Ser Gly Glu Thr Gln Arg Lys Leu Thr Phe Cys Thr
    450                 455                 460
Glu Asp Pro Glu Asn Thr Ser Ile Ser Pro Gly Arg Glu Leu Trp Phe
465                 470                 475                 480
Arg Lys Cys Arg Asp Gly Trp Arg Met Lys Asn Glu Thr Ser Pro Thr
                485                 490                 495
Val Glu Leu Pro  *
            500
```

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1035 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..1035

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```
ATG AGC AAC TCC GTT CCT CTG CTC TGT TTC TGG AGC CTC TGC TAT TGC        48
Met Ser Asn Ser Val Pro Leu Leu Cys Phe Trp Ser Leu Cys Tyr Cys
            505                 510                 515

TTT GCT GCG GGG AGC CCC GTA CCT TTT GGT CCA GAG GGA CGG CTG GAA        96
Phe Ala Ala Gly Ser Pro Val Pro Phe Gly Pro Glu Gly Arg Leu Glu
        520                 525                 530

GAT AAG CTC CAC AAA CCC AAA GCT ACA CAG ACT GAG GTC AAA CCA TCT       144
Asp Lys Leu His Lys Pro Lys Ala Thr Gln Thr Glu Val Lys Pro Ser
    535                 540                 545

GTG AGG TTT AAC CTC CGC ACC TCC AAG GAC CCA GAG CAT GAA GGA TGC       192
Val Arg Phe Asn Leu Arg Thr Ser Lys Asp Pro Glu His Glu Gly Cys
550                 555                 560                 565

TAC CTC TCC GTC GGC CAC AGC CAG CCC TTA GAA GAC TGC AGT TTC AAC       240
Tyr Leu Ser Val Gly His Ser Gln Pro Leu Glu Asp Cys Ser Phe Asn
                570                 575                 580

ATG ACA GCT AAA ACC TTT TTC ATC ATT CAC GGA TGG ACG ATG AGC GGT       288
Met Thr Ala Lys Thr Phe Phe Ile Ile His Gly Trp Thr Met Ser Gly
            585                 590                 595

ATC TTT GAA AAC TGG CTG CAC AAA CTC GTG TCA GCC CTG CAC ACA AGA       336
Ile Phe Glu Asn Trp Leu His Lys Leu Val Ser Ala Leu His Thr Arg
        600                 605                 610
```

0 0 2 9 4 3 5 3 0 5 0 2

GAG AAA GAC GCC AAT GTA GTT GTG GTT GAC TGG CTC CCC CTG GCC CAC 384
Glu Lys Asp Ala Asn Val Val Val Asp Trp Leu Pro Leu Ala His
615 620 625

CAG CTT TAC ACG GAT GCG GTC AAT AAT ACC AGG GTG GTG GGA CAC AGC 432
Gln Leu Tyr Thr Asp Ala Val Asn Asn Thr Arg Val Val Gly His Ser
630 635 640 645

ATT GCC AGG ATG CTC GAC TGG CTG CAG GAG AAG GAC GAT TTT TCT CTC 480
Ile Ala Arg Met Leu Asp Trp Leu Gln Glu Lys Asp Asp Phe Ser Leu
650 655 660

GGG AAT GTC CAC TTG ATC GGC TAC AGC CTC GGA GCG CAC GTG GCC GGG 528
Gly Asn Val His Leu Ile Gly Tyr Ser Leu Gly Ala His Val Ala Gly
665 670 675

TAT GCA GGC AAC TTC GTG AAA GGA ACG GTG GGC CGA ATC ACA GGT TTG 576
Tyr Ala Gly Asn Phe Val Lys Gly Thr Val Gly Arg Ile Thr Gly Leu
680 685 690

GAT CCT GCC GGG CCC ATG TTT GAA GGG GCC GAC ATC CAC AAG AGG CTC 624
Asp Pro Ala Gly Pro Met Phe Glu Gly Ala Asp Ile His Lys Arg Leu
695 700 705

TCT CCG GAC GAT GCA GAT TTT GTG GAT GTC CTC CAC ACC TAC ACG CGT 672
Ser Pro Asp Asp Ala Asp Phe Val Asp Val Leu His Thr Tyr Thr Arg
710 715 720 725

TCC TTC GGC TTG AGC ATT GGT ATT CAG ATG CCT GTG GGC CAC ATT GAC 720
Ser Phe Gly Leu Ser Ile Gly Ile Gln Met Pro Val Gly His Ile Asp
730 735 740

ATC TAC CCC AAT GGG GGT GAC TTC CAG CCA GGC TGT GGA CTC AAC GAT 768
Ile Tyr Pro Asn Gly Gly Asp Phe Gln Pro Gly Cys Gly Leu Asn Asp
745 750 755

GTC TTG GGA TCA ATT GCA TAT GGA ACA ATC ACA GAG GTG GTA AAA TGT 816
Val Leu Gly Ser Ile Ala Tyr Gly Thr Ile Thr Glu Val Val Lys Cys
760 765 770

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```
GAG CAT GAG CGA GCC GTC CAC CTC TTT GTT GAC TCT CTG GTG AAT CAG       864
Glu His Glu Arg Ala Val His Leu Phe Val Asp Ser Leu Val Asn Gln
    775                 780                 785
GAC AAG CCG AGT TTT GCC TTC CAG TGC ACT GAC TCC AAT CGC TTC AAA       912
Asp Lys Pro Ser Phe Ala Phe Gln Cys Thr Asp Ser Asn Arg Phe Lys
790                 795                 800                 805
AAG GGG ATC TGT CTG AGC TGC CGC AAG AAC CGT TGT AAT AGC ATT GGC       960
Lys Gly Ile Cys Leu Ser Cys Arg Lys Asn Arg Cys Asn Ser Ile Gly
                810                 815                 820
TAC AAT GCC AAG AAA ATG AGG AAC AAG AGG AAC AGC AAA ATG TAC CTA      1008
Tyr Asn Ala Lys Lys Met Arg Asn Lys Arg Asn Ser Lys Met Tyr Leu
            825                 830                 835
AAA ACC CGG GCA GGC ATG CCT TTC AGA                                 1035
Lys Thr Arg Ala Gly Met Pro Phe Arg
        840                 845
```

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 345 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

```
Met Ser Asn Ser Val Pro Leu Leu Cys Phe Trp Ser Leu Cys Tyr Cys
  1               5                  10                  15
Phe Ala Ala Gly Ser Pro Val Pro Phe Gly Pro Glu Gly Arg Leu Glu
            20                  25                  30
Asp Lys Leu His Lys Pro Lys Ala Thr Gln Thr Glu Val Lys Pro Ser
        35                  40                  45
```

SUBSTITUTE SHEET (RULE 26)

```
Val Arg Phe Asn Leu Arg Thr Ser Lys Asp Pro Glu His Glu Gly Cys
     50                  55                  60
Tyr Leu Ser Val Gly His Ser Gln Pro Leu Glu Asp Cys Ser Phe Asn
 65                  70                  75                  80
Met Thr Ala Lys Thr Phe Phe Ile Ile His Gly Trp Thr Met Ser Gly
                 85                  90                  95
Ile Phe Glu Asn Trp Leu His Lys Leu Val Ser Ala Leu His Thr Arg
            100                 105                 110
Glu Lys Asp Ala Asn Val Val Val Val Asp Trp Leu Pro Leu Ala His
        115                 120                 125
Gln Leu Tyr Thr Asp Ala Val Asn Asn Thr Arg Val Val Gly His Ser
    130                 135                 140
Ile Ala Arg Met Leu Asp Trp Leu Gln Glu Lys Asp Asp Phe Ser Leu
145                 150                 155                 160
Gly Asn Val His Leu Ile Gly Tyr Ser Leu Gly Ala His Val Ala Gly
                165                 170                 175
Tyr Ala Gly Asn Phe Val Lys Gly Thr Val Gly Arg Ile Thr Gly Leu
            180                 185                 190
Asp Pro Ala Gly Pro Met Phe Glu Gly Ala Asp Ile His Lys Arg Leu
        195                 200                 205
Ser Pro Asp Asp Ala Asp Phe Val Asp Val Leu His Thr Tyr Thr Arg
    210                 215                 220
Ser Phe Gly Leu Ser Ile Gly Ile Gln Met Pro Val Gly His Ile Asp
225                 230                 235                 240
Ile Tyr Pro Asn Gly Gly Asp Phe Gln Pro Gly Cys Gly Leu Asn Asp
                245                 250                 255
Val Leu Gly Ser Ile Ala Tyr Gly Thr Ile Thr Glu Val Val Lys Cys
            260                 265                 270
Glu His Glu Arg Ala Val His Leu Phe Val Asp Ser Leu Val Asn Gln
        275                 280                 285
```

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Asp Lys Pro Ser Phe Ala Phe Gln Cys Thr Asp Ser Asn Arg Phe Lys
290 295 300

Lys Gly Ile Cys Leu Ser Cys Arg Lys Asn Arg Cys Asn Ser Ile Gly
305 310 315 320

Tyr Asn Ala Lys Lys Met Arg Asn Lys Arg Asn Ser Lys Met Tyr Leu
325 330 335

Lys Thr Arg Ala Gly Met Pro Phe Arg
340 345

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 225 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CTG GGA TCC ATC GCC TAT GGC ACG ATC GCG GAG GTG GTG AAG TGC GAG 48
Leu Gly Ser Ile Ala Tyr Gly Thr Ile Ala Glu Val Val Lys Cys Glu
350 355 360

CAT GAG CGG GCC GTG CAT CTC TTT GTG GAC TCC CTG GTG AAC CAG GAC 96
His Glu Arg Ala Val His Leu Phe Val Asp Ser Leu Val Asn Gln Asp
365 370 375

AAG CCG AGC TTT GCC TTC CAG TGC ACA GAC TCC AAC CGC TTC AAA AAA 144
Lys Pro Ser Phe Ala Phe Gln Cys Thr Asp Ser Asn Arg Phe Lys Lys
380 385 390

GGG ATC TGT CTC AGC TGC CGG AAG AAC CGC TGT AAC GGC ATC GGC TAC 192

Gly Ile Cys Leu Ser Cys Arg Lys Asn Arg Cys Asn Gly Ile Gly Tyr
395 400 405

AAT GCT AAG AAG ACG AGG AAT AAG AGG AAC ACC 225
Asn Ala Lys Lys Thr Arg Asn Lys Arg Asn Thr
410 415 420

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Leu Gly Ser Ile Ala Tyr Gly Thr Ile Ala Glu Val Val Lys Cys Glu
1 5 10 15

His Glu Arg Ala Val His Leu Phe Val Asp Ser Leu Val Asn Gln Asp
20 25 30

Lys Pro Ser Phe Ala Phe Gln Cys Thr Asp Ser Asn Arg Phe Lys Lys
35 40 45

Gly Ile Cys Leu Ser Cys Arg Lys Asn Arg Cys Asn Gly Ile Gly Tyr
50 55 60

Asn Ala Lys Lys Thr Arg Asn Lys Arg Asn Thr
65 70 75

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 472 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```
Met Glu Ser Lys Ala Leu Leu Val Leu Thr Leu Ala Val Trp Leu Gln
1               5                  10                  15
Ser Leu Thr Ala Ser Arg Gly Gly Val Ala Ala Ala Asp Gln Arg Arg
            20                  25                  30
Asp Phe Ile Asp Ile Glu Ser Lys Phe Ala Leu Arg Thr Pro Glu Asp
        35                  40                  45
Thr Ala Glu Asp Thr Cys His Leu Ile Pro Gly Val Ala Glu Ser Val
    50                  55                  60
Ala Thr Cys His Phe Asn His Ser Ser Lys Thr Phe Met Val Ile His
65                  70                  75                  80
Gly Trp Thr Val Thr Gly Met Tyr Glu Ser Trp Val Pro Lys Leu Val
                85                  90                  95
Ala Ala Leu Tyr Lys Arg Glu Pro Asp Ser Asn Val Ile Val Val Asp
            100                 105                 110
Trp Leu Ser Arg Ala Gln Glu His Tyr Pro Val Ser Ala Gly Tyr Thr
        115                 120                 125
Lys Val Gly Gln Asp Val Ala Arg Phe Ile Asn Trp Met Glu Glu Glu
    130                 135                 140
Phe Asn Tyr Pro Leu Asp Asn Val His Leu Leu Gly Tyr Ser Leu Gly
145                 150                 155                 160
Ala His Ala Ala Gly Ile Ala Gly Ser Leu Thr Asn Lys Lys Val Asn
                165                 170                 175
Arg Ile Thr Gly Leu Asp Pro Ala Gly Pro Asn Phe Glu Tyr Ala Glu
            180                 185                 190
Ala Pro Arg Leu Ser Pro Asp Asp Ala Asp Phe Val Asp Val Leu His
        195                 200                 205
Thr Phe Thr Arg Gly Ser Pro Gly Arg Ser Ile Gly Ile Gln Lys Pro
    210                 215                 220
```

SUBSTITUTE SHEET (RULE 26)

Val Gly His Val Asp Ile Tyr Pro Asn Gly Gly Thr Phe Gln Pro Gly
225 230 235 240
Cys Asn Ile Gly Glu Ala Ile Arg Val Ile Ala Glu Arg Gly Leu Gly
245 250 255
Asp Val Asp Gln Leu Lys Cys Ser His Glu Arg Ser Ile His Leu Phe
260 265 270
Ile Asp Ser Leu Leu Asn Glu Glu Asn Pro Ser Lys Ala Tyr Arg Cys
275 280 285
Ser Ser Lys Glu Ala Phe Glu Lys Gly Leu Cys Leu Ser Cys Arg Lys
290 295 300
Asn Arg Cys Asn Asn Leu Gly Tyr Glu Ile Asn Lys Val Arg Ala Lys
305 310 315 320
Arg Ser Ser Lys Met Tyr Leu Lys Thr Arg Ser Gln Met Pro Tyr Lys
325 330 335
Val Phe His Tyr Gln Val Lys Ile His Phe Ser Gly Thr Glu Ser Glu
340 345 350
Thr His Thr Asn Gln Ala Phe Glu Ile Ser Leu Tyr Gly Thr Val Ala
355 360 365
Glu Ser Glu Asn Ile Pro Phe Thr Leu Pro Glu Val Ser Thr Asn Lys
370 375 380
Thr Tyr Ser Phe Leu Ile Tyr Thr Glu Val Asp Ile Gly Glu Leu Leu
385 390 395 400
Met Leu Lys Leu Lys Trp Lys Ser Asp Ser Tyr Phe Ser Trp Ser Asp
405 410 415
Trp Trp Ser Ser Pro Gly Phe Ala Ile Gln Lys Ile Arg Val Lys Ala
420 425 430
Gly Glu Thr Gln Lys Lys Val Ile Phe Cys Ser Arg Glu Lys Val Ser
435 440 445
His Leu Gln Lys Gly Lys Ala Pro Ala Val Phe Val Lys Cys His Asp
450 455 460

EP 0 525 742 A2

Lys Ser Leu Asn Lys Lys Ser Gly
465 470

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 499 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Asp Thr Ser Pro Leu Cys Phe Ser Ile Leu Leu Val Leu Cys Ile
1 5 10 15

Phe Ile Gln Ser Ser Ala Leu Gly Gln Ser Leu Lys Pro Glu Pro Phe
20 25 30

Gly Arg Arg Ala Gln Ala Val Glu Thr Asn Lys Thr Leu His Glu Met
35 40 45

Lys Thr Arg Phe Leu Leu Phe Gly Glu Thr Asn Gln Gly Cys Gln Ile
50 55 60

Arg Ile Asn His Pro Asp Thr Leu Gln Glu Cys Gly Phe Asn Ser Ser
65 70 75 80

Leu Pro Leu Val Met Ile Ile His Gly Trp Ser Val Asp Gly Val Leu
85 90 95

Glu Asn Trp Ile Trp Gln Met Val Ala Ala Leu Lys Ser Gln Pro Ala
100 105 110

Gln Pro Val Asn Val Gly Leu Val Asp Trp Ile Thr Leu Ala His Asp
115 120 125

His Tyr Thr Ile Ala Val Arg Asn Thr Arg Leu Val Gly Lys Glu Val
130 135 140

SUBSTITUTE SHEET (RULE 26)

```
Ala Ala Leu Leu Arg Trp Leu Glu Glu Ser Val Gln Leu Ser Arg Ser
145                 150                 155                 160
His Val His Leu Ile Gly Tyr Ser Leu Gly Ala His Val Ser Gly Phe
                165                 170                 175
Ala Gly Ser Ser Ile Gly Gly Thr His Lys Ile Gly Arg Ile Thr Gly
            180                 185                 190
Leu Asp Ala Ala Gly Pro Leu Phe Glu Gly Ser Ala Pro Ser Asn Arg
        195                 200                 205
Leu Ser Pro Asp Asp Ala Asn Phe Val Asp Ala Ile His Thr Phe Thr
    210                 215                 220
Arg Glu His Met Gly Leu Ser Val Gly Ile Lys Gln Pro Ile Gly His
225                 230                 235                 240
Tyr Asp Phe Tyr Pro Asn Gly Gly Ser Phe Gln Pro Gly Cys His Phe
                245                 250                 255
Leu Glu Leu Tyr Arg His Ile Ala Gln His Gly Phe Asn Ala Ile Thr
            260                 265                 270
Gln Thr Ile Lys Cys Ser His Glu Arg Ser Val His Leu Phe Ile Asp
        275                 280                 285
Ser Leu Leu His Ala Gly Thr Gln Ser Met Ala Tyr Pro Cys Gly Asp
    290                 295                 300
Met Asn Ser Phe Ser Gln Gly Leu Cys Leu Ser Cys Lys Lys Gly Arg
305                 310                 315                 320
Cys Asn Thr Leu Gly Tyr His Val Arg Gln Glu Pro Arg Ser Lys Ser
                325                 330                 335
Lys Arg Leu Phe Leu Val Thr Arg Ala Gln Ser Pro Phe Lys Val Tyr
            340                 345                 350
His Tyr Gln Leu Lys Ile Gln Phe Ile Asn Gln Thr Glu Thr Pro Ile
        355                 360                 365
Gln Thr Thr Phe Thr Met Ser Leu Leu Gly Thr Lys Glu Lys Met Gln
    370                 375                 380
```

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Lys Ile Pro Ile Thr Leu Gly Lys Gly Ile Ala Ser Asn Lys Thr Tyr
385 390 395 400
Ser Phe Leu Ile Thr Leu Asp Val Asp Ile Gly Glu Leu Ile Met Ile
405 410 415
Lys Phe Lys Trp Glu Asn Ser Ala Val Trp Ala Asn Val Trp Asp Thr
420 425 430
Val Gln Thr Ile Ile Pro Trp Ser Thr Gly Pro Arg His Ser Gly Leu
435 440 445
Val Leu Lys Thr Ile Arg Val Lys Ala Gly Glu Thr Gln Gln Arg Met
450 455 460
Thr Phe Cys Ser Glu Asn Thr Asp Asp Leu Leu Leu Arg Pro Thr Gln
465 470 475 480
Glu Lys Ile Phe Val Lys Cys Glu Ile Lys Ser Lys Thr Ser Lys Arg
485 490 495
Lys Ile Arg

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 465 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met Leu Pro Leu Trp Thr Leu Ser Leu Leu Leu Gly Ala Val Ala Gly
1 5 10 15
Lys Glu Val Cys Tyr Glu Arg Leu Gly Cys Phe Ser Asp Asp Ser Pro
20 25 30
Trp Ser Gly Ile Thr Glu Arg Pro Leu His Ile Leu Pro Trp Ser Pro
35 40 45

```
Lys Asp Val Asn Thr Arg Phe Leu Leu Tyr Thr Asn Glu Asn Pro Asn
    50                  55                  60
Asn Phe Gln Glu Val Ala Ala Asp Ser Ser Ser Ile Ser Gly Ser Asn
65                  70                  75                  80
Phe Lys Thr Asn Arg Lys Thr Arg Phe Ile Ile His Gly Phe Ile Asp
                85                  90                  95
Lys Gly Glu Glu Asn Trp Leu Ala Asn Val Cys Lys Asn Leu Phe Lys
            100                 105                 110
Val Glu Ser Val Asn Cys Ile Cys Val Asp Trp Lys Gly Gly Ser Arg
        115                 120                 125
Thr Gly Tyr Thr Gln Ala Ser Gln Asn Ile Arg Ile Val Gly Ala Glu
    130                 135                 140
Val Ala Tyr Phe Val Glu Phe Leu Gln Ser Ala Phe Gly Tyr Ser Pro
145                 150                 155                 160
Ser Asn Val His Val Ile Gly His Ser Leu Gly Ala His Ala Ala Gly
                165                 170                 175
Glu Ala Gly Arg Arg Thr Asn Gly Thr Ile Gly Arg Ile Thr Gly Leu
            180                 185                 190
Asp Pro Ala Glu Pro Cys Phe Gln Gly Thr Pro Glu Leu Val Arg Leu
        195                 200                 205
Asp Pro Ser Asp Ala Lys Phe Val Asp Val Ile His Thr Asp Gly Ala
    210                 215                 220
Pro Ile Val Pro Asn Leu Gly Phe Gly Met Ser Gln Val Val Gly His
225                 230                 235                 240
Leu Asp Phe Phe Pro Asn Gly Gly Val Glu Met Pro Gly Cys Lys Lys
                245                 250                 255
Asn Ile Leu Ser Gln Ile Val Asp Ile Asp Gly Ile Trp Glu Gly Thr
            260                 265                 270
Arg Asp Phe Ala Ala Cys Asn His Leu Arg Ser Tyr Lys Tyr Tyr Thr
        275                 280                 285
```

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```
Asp Ser Ile Val Asn Pro Asp Gly Phe Ala Gly Phe Pro Cys Ala Ser
    290                 295                 300
Tyr Asn Val Phe Thr Ala Asn Lys Cys Phe Pro Cys Pro Ser Gly Gly
305                 310                 315                 320
Cys Pro Gln Met Gly His Tyr Ala Asp Arg Tyr Pro Gly Lys Thr Asn
                325                 330                 335
Asp Val Gly Gln Lys Phe Tyr Leu Asp Thr Gly Asp Ala Ser Asn Phe
            340                 345                 350
Ala Arg Trp Arg Tyr Lys Val Ser Val Thr Leu Ser Gly Lys Lys Val
        355                 360                 365
Thr Gly His Ile Leu Val Ser Leu Phe Gly Asn Lys Gly Asn Ser Lys
    370                 375                 380
Gln Tyr Glu Ile Phe Lys Gly Thr Leu Lys Pro Asp Ser Thr His Ser
385                 390                 395                 400
Asn Glu Phe Asp Ser Asp Val Asp Val Gly Asp Leu Gln Met Val Lys
                405                 410                 415
Phe Ile Trp Tyr Asn Asn Val Ile Asn Pro Thr Leu Pro Arg Val Gly
            420                 425                 430
Ala Ser Lys Ile Ile Val Glu Thr Asn Val Gly Lys Gln Phe Asn Phe
        435                 440                 445
Cys Ser Pro Glu Thr Val Arg Glu Glu Val Leu Leu Thr Leu Thr Pro
    450                 455                 460
Cys
465
```

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Gly Pro Glu Gly Arg Leu Glu Asp Lys Leu His Lys Pro Lys Ala Thr
1 5 10 15

Cys

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TTTTTTTTTT TGA 13

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GATCAATCGC 10

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TAGGACATGC ACAGTGTAAT CTG 23

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GATTGTGCTG GCCACTTCTC 20

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GACACTCCAG GGACTGAAG 19

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Oligonucleotide"

(ix) FEATURE:

(A) NAME/KEY: modified_base

(B) LOCATION: 36

(D) OTHER INFORMATION: /mod_base= i

(ix) FEATURE:

(A) NAME/KEY: modified_base

(B) LOCATION: 37

(D) OTHER INFORMATION: /mod_base= i

(ix) FEATURE:

(A) NAME/KEY: modified_base

(B) LOCATION: 41

(D) OTHER INFORMATION: /mod_base= i

(ix) FEATURE:

(A) NAME/KEY: modified_base

(B) LOCATION: 42

(D) OTHER INFORMATION: /mod_base= i

(ix) FEATURE:

(A) NAME/KEY: modified_base

(B) LOCATION: 46

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(D) OTHER INFORMATION: /mod_base= i

(ix) FEATURE:

(A) NAME/KEY: modified_base

(B) LOCATION: 47

(D) OTHER INFORMATION: /mod_base= i

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CUACUACUAC UAGGCCACGC GTCGACTAGT ACGGGNNGGG NNGGGNNG 48

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CACACACAGG CCACGCGTCG ACTAGTAC 28

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ACCACCATGG AGAGCAAAGC CCTG 24

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CCAGTTTCAG CCTGACTTCT TATTC 25

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GGCTGTGGAC TCAACGATGT C 21

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CCGGGTGGGT AGGTACATTT TG 22

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GGGGGTGACT TCCAGCCAGG CTGTG 25

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

AACTCTGAAA GGCATGCCTG CCCGG 25

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TGAAGGTCGG AGTCAACGGA TTTGGT 26

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CATGTGGGCC ATGAGGTCCA CCAC 24

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